

*Amendments to the Claims:*

Please **cancel** claims 1-38 without prejudice to or disclaimer of the underlying subject matter, and please **add** the following claims 39-91:

1-38. (Cancelled)

39. (New) A DNA construct comprising a coding sequence for a *Cuphea* KAS factor A protein, and one or more coding sequences for a plant medium-chain thioesterase protein.

40. (New) The DNA construct according to claim 39, wherein said one or more coding sequences for a plant medium-chain thioesterase protein are selected from the group consisting of *Cuphea hookeriana* FatB2, *Cuphea pulcherrima* FatB1, and *Umbellularia californica* FatB1.

41. (New) The DNA construct according to claim 39, wherein said coding sequence for a *Cuphea* KAS factor A protein is set forth in a sequence selected from the group consisting of SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 13, and SEQ ID NO: 15.

42. (New) The DNA construct according to claim 39, wherein said coding sequence for a *Cuphea* KAS factor A protein is set forth in SEQ ID NO: 5.

43. (New) A DNA construct comprising a coding sequence for a *Cuphea* KAS factor A protein, and a coding sequences for *Garcinia mangostana* FatA1 thioesterase protein.

44. (New) An improved method for producing medium-chain fatty acids in transgenic plant seeds by expression of one or more plant medium-chain thioesterase proteins heterologous to said transgenic plant,

the improvement comprising expression of a plant synthase factor protein heterologous to said transgenic plant in conjunction with expression of said one or more plant medium-chain thioesterase proteins, whereby the percentage of medium-chain fatty acids produced in seeds expressing both a plant synthase factor protein and one or more plant medium-chain thioesterase proteins is increased as compared to the percentage of medium-chain fatty acids produced in seeds expressing only said one or more plant medium-chain thioesterase proteins.

45. (New) The method of Claim 44 wherein said one or more plant medium-chain thioesterase proteins is a *Cuphea hookeriana* FatB2 protein.

46. (New) The method of Claim 44 wherein said one or more plant medium-chain thioesterase proteins is a *Cuphea pulcherrima* FatB1 protein.

47. (New) The method of Claim 44 wherein said one or more plant medium-chain thioesterase proteins is an *Umbellularia californica* FatB1 protein.

48. (New) The method of Claim 44 wherein said one or more plant medium-chain thioesterase proteins is a *Cuphea hookeriana* FatB2 protein and a *Cuphea pulcherrima* FatB1 protein.

49. (New) The method of Claim 44 wherein said plant synthase factor protein is a KAS factor A protein from a *Cuphea* species.

50. (New) The method of Claim 49 wherein said *Cuphea* species is *C. hookeriana* or *C. pulcherrima*.

51. (New) The method of Claim 50 wherein said KAS factor A protein comprises a coding sequence as set forth in SEQ ID NO:5.

52. (New) The method of Claim 50 wherein said KAS factor A protein comprises a coding sequence encoding an amino acid sequence as set forth in SEQ ID NO:6.

53. (New) The method of Claim 50 wherein said synthase factor A protein comprises a coding sequence encoding an amino acid sequence set forth in residues 125-466 of SEQ ID NO:6.

54. (New) A method of altering the medium-chain fatty acid composition in plant seeds expressing one or more heterologous plant medium-chain thioesterase proteins, wherein said method comprises

providing for expression of a plant synthase factor protein heterologous to said transgenic plant in conjunction with expression of a plant medium-chain thioesterase protein heterologous to said transgenic plant, whereby the composition of medium-chain fatty acids produced in said seeds is modified as compared to the composition of medium-chain fatty acids produced in seeds expressing said plant medium-chain thioesterase protein in the absence of expression of said plant synthase factor protein.

55. (New) The method of Claim 54 wherein said one or more heterologous plant medium-chain thioesterase proteins is a *Cuphea hookeriana* FatB2 protein.

56. (New) The method of Claim 54 wherein said one or more heterologous plant medium-chain thioesterase proteins is a *Cuphea pulcherrima* FatB1 protein.

57. (New) The method of Claim 54 wherein said one or more heterologous plant medium-chain thioesterase proteins is a *Umbellularia californica* FatB1 protein.

58. (New) The method of Claim 54 wherein said one or more plant medium-chain thioesterase proteins is a *Cuphea hookeriana* FatB2 protein and a *Cuphea pulcherrima* FatB1 protein.

59. (New) The method of Claim 54 wherein said plant synthase factor protein is a KAS factor A protein from a *Cuphea* species.

60. (New) The method of Claim 59 wherein said *Cuphea* species is *C. hookeriana* or *C. pulcherrima*.

61. (New) The method of Claim 54 wherein said fatty acid composition is enriched for C10 fatty acids.

62. (New) The method of Claim 54 wherein said fatty acid composition is enriched for C12 fatty acids.

63. (New) The method of Claim 54 wherein said fatty acid composition is enriched for at least one medium chain fatty acid and at least one other medium chain fatty acid is decreased.

64. (New) The method of Claim 63 wherein said enriched fatty acid is C12 and said decreased fatty acid is C14.

65. (New) The method of claim 54, wherein said altered fatty acid composition comprises an increased ratio of C10 fatty acids to C8 fatty acids.

66. (New) The method of claim 54, wherein said altered fatty acid composition comprises an increased total content of C10 fatty acids and C8 fatty acids.

67. (New) A transformed plant comprising a coding sequence for a thioesterase protein, and a coding sequence for a KAS factor A protein, wherein said coding sequence for a KAS factor A protein is derived from a species from the genus *Cuphea*.

68. (New) The transformed plant of claim 67, wherein said thioesterase protein is selected from the group consisting of *Cuphea hookeriana* FatB2, *Cuphea pulcherrima* FatB1, *Umbellularia californica* FatB1, and *Garcinia mangostana* FatA1.

69. (New) The transformed plant of claim 67, wherein said thioesterase protein is *Cuphea hookeriana* FatB2.

70. (New) The transformed plant of claim 67, wherein said thioesterase protein is *Cuphea pulcherrima* FatB1.

71. (New) The transformed plant of claim 67, wherein said thioesterase protein is *Umbellularia californica* FatB1.

72. (New) The transformed plant of claim 67, wherein said coding sequence for said KAS factor A protein is set forth in a sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:13 and SEQ ID NO:15.

73. (New) The transformed plant of claim 67, wherein said coding sequence for said KAS factor A protein is set forth in SEQ ID NO:5.

74. (New) The transformed plant of claim 67, wherein said KAS factor A protein has the amino acid sequence set forth in a sequence selected from the group consisting of SEQ ID NO:6, residues 125-466 of SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:14, and residues 127-546 of SEQ ID NO:14.

75. (New) The transformed plant of claim 67, wherein said KAS factor A protein has the amino acid sequence set forth in SEQ ID NO:6.

76. (New) The transformed plant of claim 67, wherein said KAS factor A protein has the amino acid sequence set forth in residues 125-466 of SEQ ID NO:6.

77. (New) The transformed plant of claim 67, wherein said transformed plant has an altered composition of medium-chain fatty acids relative to an untransformed plant.

78. (New) The transformed plant of claim 77, wherein said fatty acid composition is enriched for C10 fatty acids.

79. (New) The transformed plant of claim 77, wherein said fatty acid composition is enriched for C12 fatty acids.

80. (New) The transformed plant of claim 77, wherein said fatty acid composition is enriched for at least one medium chain fatty acid and at least one other medium chain fatty acid is decreased.

81. (New) The transformed plant of claim 77, wherein said enriched fatty acid is C12 and said decreased fatty acid is C14.

82. (New) The transformed plant of claim 77, wherein said transformed plant has an increased ratio of C10 fatty acids to C8 fatty acids relative to an untransformed plant.

83. (New) The transformed plant of claim 77, wherein said transformed plant has an increased total content of C10 fatty acids and C8 fatty acids relative to an untransformed plant.

84. (New) A transformed plant comprising a coding sequence for a *Cuphea hookeriana* FatB2, a coding sequence for a *Cuphea pulcherrima* FatB1, and a coding sequence for a KAS factor A protein, wherein said coding sequence for a KAS factor A protein is derived from a species from the genus *Cuphea*.

85. (New) The transformed plant of claim 84, wherein said transformed plant has an altered composition of medium-chain fatty acids relative to an untransformed plant.

86. (New) The transformed plant of claim 85, wherein said fatty acid composition is enriched for C10 fatty acids.

87. (New) The transformed plant of claim 85, wherein said fatty acid composition is enriched for C12 fatty acids.

88. (New) The transformed plant of claim 85, wherein said fatty acid composition is enriched for at least one medium chain fatty acid and at least one other medium chain fatty acid is decreased.

89. (New) The transformed plant of claim 85, wherein said enriched fatty acid is C12 and said decreased fatty acid is C14.

90. (New) The transformed plant of claim 85, wherein said transformed plant has an increased ratio of C10 fatty acids to C8 fatty acids relative to an untransformed plant.



91. (New) The transformed plant of claim 85, wherein said transformed plant has an increased total content of C10 fatty acids and C8 fatty acids relative to an untransformed plant.